

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK

(ii) TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear
(B) STREET: 620 Newport Center Drive 16th Floor
(C) CITY: Newport Beach
(D) STATE: CA
(E) COUNTRY: U.S.A.
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/833,752
(B) FILING DATE: 9-APR-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Altman, Daniel E
(B) REGISTRATION NUMBER: 34,115
(C) REFERENCE/DOCKET NUMBER:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 240..791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAAGCTAG CAGCAAACCT	60
TCCCTTCACT ACAAAAACCTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC	120
TATGTAGGCA ATTAAAAACC TATTGATGTA TAAAACAGTT TGCAATTGATG GAGGGCAACT	180
AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGAAACAAG	239
ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA	287
Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr	
1 5 10 15	
TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC	335
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu	
20 25 30	
CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC	383
Ile Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn	
35 40 45	
ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG	431
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met	
50 55 60	
ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT	479
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu	
65 70 75 80	
CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT	527
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe	
85 90 95	
GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC	575
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe	
100 105 110	
TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG	623
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu	
115 120 125	
GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT	671
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe	
130 135 140	
GGG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT	719
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser	
145 150 155 160	
CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC	767
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr	
165 170 175	
ACC TGC AGC TCT CAT TTT CCA TAC A	792
Thr Cys Ser Ser His Phe Pro Tyr	
180	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 240..1295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GAATTCCCCC AACAGAGCCA AGCTCTCCAT	CTAGTGGACA GGGAAAGCTAG CAGCAAACCT	60
TCCCTTCACT ACAAAACTTC ATTGCTTGGC	CAAAAAGAGA GTTAATTCAA TGTAGACATC	120
TATGTAGGCA ATTAAGAAC TATTGATGTA	AAAAACAGTT TGCATTCATG GAGGGCAACT	180
AAATACATTC TAGGACTTTA TAAAAGATCA	CTTTTATTT ATGCACAGGG TGGAACAAG	239
ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA		287
Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr		
1 5 10 15		
TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC		335
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu		
20 25 30		
CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC		383
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn		
35 40 45		
ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG		431
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met		
50 55 60		
ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT		479
Thr Asp Ile Tyr Leu Leu Asn Ala Ile Ser Asp Leu Phe Phe Leu		
65 70 75 80		
CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT		527
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Gln Trp Asp Phe		
85 90 95		
GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC		575
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe		
100 105 110		
TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG		623
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu		
115 120 125		
GCT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT		671
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe		
130 135 140		
GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT		719
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser		
145 150 155 160		
CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC		767
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr		
165 170 175		

ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT CAA TTC TGG AAG AAT	815
Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn	
180 185 190	
TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG GTC CTG CCG CTG CTT	863
Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu	
195 200 205	
GTC ATG GTG ATC TGC TAC TCG GGA ATC CTA AAA ACT CTG CTT CGG TGT	911
Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys	
210 215 220	
CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG CTT ATC TTC ACC ATC	959
Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile	
225 230 235 240	
ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC AAC ATT GTC CTT CTC	1007
Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu	
245 250 255	
CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT	1055
Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser	
260 265 270	
AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG ACT CTT GGG ATG ACG	1103
Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr	
275 280 285	
CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC	1151
His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe	
290 295 300	
AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCC AAA CGC TTC	1199
Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe	
305 310 315 320	
TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGC	1247
Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser	
325 330 335	
TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG	1295
Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu	
340 345 350	
TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG TGCACATGGC TTAGTTTCA	1355
TACACAGCCT GGGCTGGGG TNGGTTGGNN GAGGTCTTTT TAAAAAGGAA GTTACTGTTA	1415
TAGAGGGTCT AAGATTTCATC CATTATTTG GCATCTGTTT AAAGTAGATT AGATCCGAAT	1475
TC	1477

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 240..884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAAGCTAG CAGCAAACCT	60
TCCCTTCACT ACAAAACTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC	120
TATGTAGGCA ATTAAAAACC TATTGATGTA TAAAACAGTT TGCATTCATG GAGGGCAACT	180
AAATAACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGAACAAG	239
ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA	287
Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr	
1 5 10 15	
TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC	335
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu	
20 25 30	
CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC	383
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn	
35 40 45	
ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG	431
Met Leu Val Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met	
50 55 60	
ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT	479
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu	
65 70 75 80	
CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT	527
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe	
85 90 95	
GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC	575
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe	
100 105 110	
TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG	623
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu	
115 120 125	
GCT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT	671
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe	
130 135 140	
GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GCT GTG TTT GCG TCT	719
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser	
145 150 155 160	
CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC	767
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr	
165 170 175	
ACC TGC AGC TCT CAT TTT CCA TAC ATT AAA GAT AGT CAT CTT GGG GCT	815
Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala	
180 185 190	
GGT CCT GCC GCT GCT TGT CAT GGT CAT CTG CTA CTC GGG AAT CCT AAA	863
Gly Pro Ala Ala Ala Cys His Gly His Leu Leu Leu Gly Asn Pro Lys	
195 200 205	
AAC TCT GCT TCG GTG TCG AAA TGAGAAGAAG AGGCACAGGG CTGTGAGGCT	914
Asn Ser Ala Ser Val Ser Lys	
210 215	
TATCTTCACC ATCATGATTG TTTATTTCT CTTCTGGCT CCCTACAACA TTGTCCTTCT	974

CCTGAACACC	TTCCAGGAAT	TCTTGGCCT	GAATAATTGC	AGTAGCTCTA	ACAGGTTGGA	1034
CCAAGCTATG	CAGGTGACAG	AGACTCTTGG	GATGACGCAC	TGCTGCATCA	ACCCCACATC	1094
CTATGCCCTT	GTCGGGGAGA	AGTTCAGAAA	CTACCTCTTA	GTCTTCTTCC	AAAAGCACAT	1154
TGCCAAACGC	TTCTGCAAAT	GCTGTTCTAT	TTTCCAGCAA	GAGGCTCCCG	AGCGAGCAAG	1214
CTCAGTTAC	ACCCGATCCA	CTGGGGAGCA	GGAAATATCT	GTGGGCTTGT	GACACGGACT	1274
CAAGTGGGCT	GGTGACCCAG	TCAGAGTTGT	GCACATGGCT	TAGTTTCAT	ACACAGCCTG	1334
GGCTGGGGGT	GGTTGGGAGG	TCTTTTAA	AAGGAAGTTA	CTGTTATAGA	GGGTCTAAGA	1394
TTCATCCATT	TATTTGGCAT	CTGTTAAAG	TAGATTAGAT	CCGAATT		1442

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
      1           5           10          15
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
      20          25          30
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
      35          40          45
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
      50          55          60
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
      65          70          75          80
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
      85          90          95
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
      100         105         110
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
      115         120         125
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
      130         135         140
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
      145         150         155         160
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
      165         170         175
Thr Cys Ser Ser His Phe Pro Tyr
      180

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
1 5 10 15
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35 40 45
Met Leu Val Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
50 55 60
Thr Asp Ile Tyr Leu Leu Asn Ala Ile Ser Asp Leu Phe Phe Leu
65 70 75 80
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Gln Trp Asp Phe
85 90 95
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115 120 125
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130 135 140
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
165 170 175
Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
180 185 190
Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
195 200 205
Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
210 215 220
Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
225 230 235 240
Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
245 250 255
Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
260 265 270
Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
275 280 285
His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
290 295 300
Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
305 310 315 320
Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
325 330 335
Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
340 345 350

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
1 5 10 15
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
20 25 30
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
35 40 45
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
50 55 60
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65 70 75 80
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
85 90 95
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
100 105 110
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
115 120 125
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130 135 140
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145 150 155 160
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
165 170 175
Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala
180 185 190
Gly Pro Ala Ala Ala Cys His Gly His Leu Leu Leu Gly Asn Pro Lys
195 200 205
Asn Ser Ala Ser Val Ser Lys
210 215

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
 1 5 10 15
 Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
 20 25 30
 His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
 35 40 45
 Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
 50 55 60
 Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
 65 70 75 80
 Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Ile Ile Thr Leu Pro
 85 90 95
 Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
 100 105 110
 Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
 115 120 125
 Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
 130 135 140
 Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
 145 150 155 160
 Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
 165 170 175
 Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
 180 185 190
 Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
 195 200 205
 Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 210 215 220
 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 225 230 235 240
 Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 245 250 255
 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 260 265 270
 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Ile Gln
 275 280 285
 Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 290 295 300
 Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg Tyr Ile Ser Val Phe Phe
 305 310 315 320
 Arg Lys His Ile Xaa Xaa Xaa Phe Cys Lys Gln Cys Pro Val Phe Tyr
 325 330 335
 Arg Glu Thr Val Asp Gly Val Thr Ser Thr Asn Thr Pro Ser Thr Gly
 340 345 350
 Glu Gln Glu Val Ser Ala Gly Leu
 355 360

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Thr Ser Ile Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr
1 5 10 15
Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu
20 25 30
Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly
35 40 45
Leu Ile Gly Asn Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
50 55 60
Ile Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65 70 75 80
Leu Leu Phe Ile Val Thr Leu Pro Phe Trp Thr His Tyr Val Arg Gly
85 90 95
His Asn Trp Val Phe Gly His Gly Met Cys Asn Leu Ile Ser Gly Phe
100 105 110
Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
115 120 125
Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Ile Arg Ala
130 135 140
Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Ile
145 150 155 160
Ala Val Ile Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
165 170 175
Leu Phe Glu Glu Thr Ile Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
180 185 190
Tyr Ser Trp Arg His Phe His Thr Ile Arg Met Thr Ile Phe Cys Leu
195 200 205
Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
210 215 220
Thr Leu Leu Arg Cys Pro Xaa Xaa Xaa Lys Tyr Lys Ala Ile Arg Leu
225 230 235 240
Ile Phe Val Ile Met Ala Val Phe Phe Ile Glu Trp Thr Pro Tyr Asn
245 250 255
Val Ala Ile Leu Ile Ser Ser Tyr Gln Ser Leu Leu Phe Gly Asn Asn
260 265 270
Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Ile Val Thr Glu Val
275 280 285
Ile Ala Tyr Ser His Cys Cys Met Asn Glu Val Ile Tyr Ala Phe Val
290 295 300
Gly Glu Arg Phe Arg Lys Tyr Ile Arg His Phe Phe His Arg His Leu
305 310 315 320
Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Xaa Xaa Xaa Ile
325 330 335
Glu Arg Ile Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Ile Ser
340 345 350
Ile Val Phe

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe
 1 5 10 15
 Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
 20 25 30
 Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
 35 40 45
 Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
 50 55 60
 Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80
 Leu Leu Phe Ile Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
 85 90 95
 Asp Asp Trp Val Phe Gly Asp Ala Met Cys Lys Ile Ile Ser Gly Phe
 100 105 110
 Tyr Tyr Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
 115 120 125
 Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Ile Arg Ala
 130 135 140
 Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Ile Ile Trp Ala Ile
 145 150 155 160
 Ala Ile Ile Ala Ser Met Pro Gly Leu Tyr Phe Ser Lys Thr Gln Trp
 165 170 175
 Glu Phe Thr His His Thr Cys Ser Leu His Phe Pro His Glu Ser Leu
 180 185 190
 Arg Glu Trp Lys Leu Phe Gln Ala Leu Lys Leu Asn Leu Phe Gly Leu
 195 200 205
 Val Leu Pro Leu Leu Val Met Ile Ile Cys Tyr Ile Gly Ile Ile Lys
 210 215 220
 Ile Leu Leu Arg Arg Pro Asn Glu Lys Lys Ser Lys Ala Val Arg Leu
 225 230 235 240
 Ile Phe Val Ile Met Ile Ile Phe Phe Leu Phe Trp Ile Pro Tyr Asn
 245 250 255
 Leu Thr Ile Ile Ile Ser Val Phe Gln Asp Phe Leu Phe Thr His Glu
 260 265 270
 Cys Glu Gln Ser Arg His Leu Asp Leu Ala Val Gln Val Thr Glu Val
 275 280 285
 Ile Ala Tyr Thr His Cys Cys Val Asn Glu Val Ile Tyr Ala Phe Val
 290 295 300

Gly	Glu	Arg	Phe	Arg	Lys	Tyr	Ile	Arg	Gln	Leu	Glu	His	Arg	Arg	Val
305					310					315					320
Ala	Val	His	Leu	Val	Lys	Trp	Leu	Pro	Phe	Leu	Ser	Val	Asp	Arg	Ile
					325					330					335
Glu	Arg	Val	Ser	Ser	Thr	Ser	Pro	Ser	Thr	Gly	Glu	His	Glu	Ile	Ser
					340					345					350
Ala	Gly	Phe													
		355													

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Asn	Pro	Thr	Asp	Ile	Ala	Asp	Thr	Thr	Leu	Asp	Glu	Ser	Ile	Tyr
1				5					10					15	
Ser	Asn	Tyr	Tyr	Leu	Tyr	Glu	Ser	Ile	Pro	Lys	Pro	Cys	Thr	Lys	Glu
				20				25						30	
Gly	Ile	Lys	Ala	Phe	Gly	Glu	Leu	Phe	Leu	Pro	Pro	Leu	Tyr	Ser	Leu
				35				40					45		
Val	Glu	Val	Phe	Gly	Leu	Ile	Gly	Asn	Ser	Val	Val	Val	Leu	Val	Leu
				50				55					60		
Phe	Lys	Tyr	Lys	Arg	Ile	Arg	Ser	Met	Thr	Asp	Val	Tyr	Leu	Leu	Asn
65					70					75				80	
Leu	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Val	Phe	Ser	Leu	Pro	Phe	Trp	Gly
					85					90				95	
Tyr	Tyr	Ala	Ala	Asp	Gln	Trp	Val	Phe	Gly	Leu	Gly	Ile	Cys	Lys	Met
					100				105				110		
Ile	Ser	Trp	Met	Tyr	Leu	Val	Gly	Phe	Tyr	Ser	Gly	Ile	Phe	Phe	Val
					115			120					125		
Met	Ile	Met	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Glu
						130		135				140			
Xaa	Xaa	Xaa	Ala	Arg	Thr	Ile	Ile	Tyr	Gly	Val	Ile	Thr	Ser	Leu	Ala
						145		150			155			160	
Thr	Trp	Ser	Val	Ala	Val	Phe	Ala	Ser	Leu	Pro	Gly	Phe	Ile	Phe	Ser
						165			170				175		
Thr	Cys	Tyr	Thr	Glu	Arg	Asn	His	Thr	Tyr	Cys	Lys	Thr	Lys	Tyr	Ser
						180			185				190		
Leu	Asn	Ser	Thr	Thr	Trp	Lys	Val	Leu	Ser	Ser	Leu	Glu	Ile	Asn	Ile
						195		200				205			
Leu	Gly	Leu	Val	Ile	Pro	Leu	Gly	Ile	Met	Leu	Phe	Cys	Tyr	Ser	Met
					210		215				220				
Ile	Ile	Arg	Thr	Leu	Gln	His	Cys	Lys	Asn	Glu	Lys	Lys	Asn	Lys	Ala
					225		230			235				240	
Val	Lys	Met	Ile	Phe	Ala	Val	Val	Val	Leu	Phe	Gly	Phe	Trp	Thr	

245	250	255
Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val		
260	265	270
Ile Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala		
275	280	285
Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr		
290	295	300
Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Ile Gln Leu Phe Lys		
305	310	315
Xaa Xaa Xaa Gly Leu Phe Val Ile Cys Gln Tyr Cys Gly Leu Leu Gln		
325	330	335
Ile Tyr Ser Ala Asp Thr Pro Ser Ser Tyr Thr Gln Ser Thr Met		
340	345	350
Asp His Asp Leu His Asp Ala Leu		
355	360	

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn			
1	5	10	15
Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu			
20	25	30	
Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys			
35	40	45	
Arg Asn Glu Lys Lys Arg			
50			

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTCCATACA GTCAGTATCA ATTCTGGAAG AATTCCAGA CATTAAGAT AGTCATCTG	60
GGGCTGGTCC TGCCGCTGCT TGTCTGGTC ATCTGCTACT CGGGAATCCT AAAAACTCTG	120
CTTCGGTGTC GAAATGAGAA GAAGAGG	147

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala Gly Pro Ala Ala Ala
1 5 10 15
Cys His Gly His Leu Leu Leu Gly Asn Pro Lys Asn Ser Ala Ser Val
20 25 30
Ser Lys

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCGAGGATCC AAGATGGATT ATCAAGT

27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGATCTAGA GCCATGTGCA CAACTCT

27

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTGGCTGTC GTCCATGCTG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGATCTAGA GCCATGTGCA CAACTCT

27